

PATENT

Attorney Docket No. 14448-00017

IN THE UNITED STATES
PATENT AND TRADEMARK OFFICE

Application of: LAU, Lester F.

Continuation of:

Serial No.: 09/142,569

Filed: April 2, 1999

For: EXTRACELLULAR MATRIX
SIGNALLING MOLECULES

Group Art Unit: 1632

Examiner: J. T. Voitach

CERTIFICATE OF MAILING BY "EXPRESS MAIL"

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Date of Deposit January 22, 2002

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" Service under 37 CFR §1.10 on the date indicated above and is addressed to the Commissioner of Patents and Trademarks, Attention: Assistant Commissioner for Patents, Washington, D.C. 20231

Theresa A. Barnstable

(Typed or printed name of person mailing)

Theresa A. Barnstable
(Signature of person mailing)

STATEMENT PURSUANT TO 37 C.F.R. § 1.821(g)

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that the content of the paper copy of the Sequence Listing, and the computer readable copy of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821-1.825, are the same and include no new matter.

Respectfully submitted,

By:

David W. Clough
David W. Clough, Ph.D.
Registration No. 36,107
Attorney for Applicants

January 22, 2002
KATTEN MUCHIN ZAVIS
525 West Monroe Street, Suite 1600
Chicago, Illinois 60661-3693
Telephone: 312/902-5464
Fax: 312/577-8736

10053753-012002

02/15

#2



OIPPE

RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/10/053,753

TIME: 16:04:11

Input Set : A:\50013825_1.RTF

Output Set: N:\CRF3\02142002\J053753.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: Lau, Lester F.
- 8 (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- 10 (iii) NUMBER OF SEQUENCES: 17
- 12 (iv) CORRESPONDENCE ADDRESS:
 - 13 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - 14 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - 15 (C) CITY: Chicago
 - 16 (D) STATE: Illinois
 - 17 (E) COUNTRY: United States of America
 - 18 (F) ZIP: 60606-6402

20 (v) COMPUTER READABLE FORM:

- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

- C--> 27 (A) APPLICATION NUMBER: US/10/053,753
- C--> 28 (B) FILING DATE: 22-Jan-2002
- 29 (C) CLASSIFICATION:

31 (viii) ATTORNEY/AGENT INFORMATION:

- 32 (A) NAME: Clough, David W.
- 33 (B) REGISTRATION NUMBER: 36,107
- 34 (C) REFERENCE/DOCKET NUMBER: 28758/33766

36 (ix) TELECOMMUNICATION INFORMATION:

- 37 (A) TELEPHONE: 312/474-6300
- 38 (B) TELEFAX: 312/474-0448
- 39 (C) TELEX: 25-3856

41 (2) INFORMATION FOR SEQ ID NO: 1:

43 (i) SEQUENCE CHARACTERISTICS:

- 44 (A) LENGTH: 1480 base pairs
- 45 (B) TYPE: nucleic acid
- 46 (C) STRANDEDNESS: single
- 47 (D) TOPOLOGY: linear

49 (ii) MOLECULE TYPE: protein

51 (ix) FEATURE:

- 52 (A) NAME/KEY: CDS
- 53 (B) LOCATION: 180..1316

55 (ix) FEATURE:

- 56 (A) NAME/KEY: misc_feature
- 57 (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61	CGAGAGCGCC	CCAGAGAAGC	GCCTGCAATC	TCTGCGCCTC	CTCCGCCAGC	ACCTCGAGAG	60
63	AAGGACACCC	GCCGCCTCGG	CCCTCGCCTC	ACCGCACTCC	GGGCGCATTT	GATCCCGCTG	120
65	CTCGCCGGCT	TGTTGGTTCT	GTGTCGCCGC	GCTCGCCCCG	GTTCTCTCTG	CGCGCCACA	179
67	ATG AGC TCC	AGC ACC TTC	AGG ACG CTC	GCT GTC GCC	GTC ACC CTT	CTC	227
68	Met Ser Ser	Ser Thr Phe	Arg Thr Leu	Ala Val Ala	Val Thr Leu	Leu	
69	1	5	10	15			
71	CAC TTG ACC	AGA CTG GCG	CTC TCC ACC	TGC CCC GCC	GCC TGC CAC	TGC	275
72	His Leu Thr	Arg Leu Ala	Leu Ser Thr	Cys Pro Ala	Ala Cys His	Cys	
73		20	25	30			
75	CCT CTG GAG	GCA CCC AAG	TGC GCC CCG	GGA GTC GGG	TTG GTC CGG	GAC	323
76	Pro Leu Glu	Ala Pro Lys	Cys Ala Pro	Gly Val Gly	Leu Val Arg	Asp	
77		35	40	45			
79	GGC TGC GGC	TGC TGT AAG	GTC TGC GCT	AAA CAA CTC	AAC GAG GAC	TGC	371
80	Gly Cys Gly	Cys Cys Lys	Val Cys Ala	Lys Gln Leu	Asn Glu Asp	Cys	
81	50	55	60				
83	AGC AAA ACT	CAG CCC TGC	GAC CAC ACC	AAG GGG TTG	GAA TGC AAT	TTC	419
84	Ser Lys Thr	Gln Pro Cys	Asp His Thr	Lys Gly Leu	Glu Cys Asn	Phe	
85	65	70	75	80			
87	GGC GCC AGC	TCC ACC GCT	CTG AAA GGG	ATC TGC AGA	GCT CAG TCA	GAA	467
88	Gly Ala Ser	Ser Thr Ala	Leu Lys Gly	Ile Cys Arg	Ala Gln Ser	Glu	
89		85	90	95			
91	GGC AGA CCC	TGT GAA TAT	AAC TCC AGA	ATC TAC CAA	AAC GGG GAA	AGC	515
92	Gly Arg Pro	Cys Glu Tyr	Asn Ser Arg	Ile Tyr Gln	Asn Gly Glu	Ser	
93		100	105	110			
95	TTC CAG CCC	AAC TGT AAA	CAC CAG TGC	ACA TGT ATT	GAT GGC GCC	GTG	563
96	Phe Gln Pro	Asn Cys Lys	His Gln Cys	Thr Cys Ile	Asp Gly Ala	Val	
97		115	120	125			
99	GGC TGC ATT	CCT CTG TGT	CCC CAA GAA	CTG TCT CTC	CCC AAT CTG	GGC	611
100	Gly Cys Ile	Pro Leu Cys	Pro Gln Glu	Leu Ser Leu	Pro Asn Leu	Gly	
101		130	135	140			
103	TGT CCC AAC	CCC CGG CTG	GTG AAA GTC	AGC GGG CAG	TGC TGT GAA	GAG	659
104	Cys Pro Asn	Pro Arg Leu	Val Lys Val	Ser Gly Gln	Cys Cys Glu	Glu	
105	145	150	155	160			
107	TGG GTT TGT	GAT GAA GAC	AGC ATT AAG	GAC TCC CTG	GAC GAC CAG	GAT	707
108	Trp Val Cys	Asp Glu Asp	Ser Ile Lys	Asp Ser Leu	Asp Asp Gln	Asp	
109		165	170	175			
111	GAC CTC CTC	GGA CTC GAT	GCC TCG GAG	GTG GAG TTA	ACG AGA AAC	AAT	755
112	Asp Leu Leu	Gly Leu Asp	Ala Ser Glu	Val Glu Leu	Thr Arg Asn	Asn	
113		180	185	190			
115	GAG TTA ATC	GCA ATT GGA	AAA GGC AGC	TCA CTG AAG	AGG CTT CCT	GTC	803
116	Glu Leu Ile	Ala Ile Gly	Lys Gly Ser	Ser Leu Lys	Arg Leu Pro	Val	
117		195	200	205			
119	TTT GGC ACC	GAA CCG CGA	GTT CTT TTC	AAC CCT CTG	CAC GCC CAT	GGC	851
120	Phe Gly Thr	Glu Pro Arg	Val Leu Phe	Asn Pro Leu	His Ala His	Gly	
121		210	215	220			
123	CAG AAA TGC	ATC GTT CAG	ACC ACG TCT	TGG TCC CAG	TGC TCC AAG	AGC	899
124	Gln Lys Cys	Ile Val Gln	Thr Thr Ser	Trp Ser Gln	Cys Ser Lys	Ser	
125	225	230	235	240			
127	TGC GGA ACT	GGC ATC TCC	ACA CGA GTT	ACC AAT GAC	AAC CCA GAG	TGC	947

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128 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
129                245                250                255
131 CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA      995
132 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
133                260                265                270
135 CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG      1043
136 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
137                275                280                285
139 AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC      1091
140 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
141                290                295                300
143 AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC      1139
144 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
145 305                310                315                320
147 TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA      1187
148 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
149                325                330                335
151 GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA      1235
152 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
153                340                345                350
155 TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC      1283
156 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
157                355                360                365
159 AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT      1336
160 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
161                370                375
163 AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG      1396
165 AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAACTGCC AAGGGGCTGA      1456
167 TGTGGACGGA CAGCAGCGCA GCCG      1480
169 (2) INFORMATION FOR SEQ ID NO: 2:
171     (i) SEQUENCE CHARACTERISTICS:
172         (A) LENGTH: 379 amino acids
173         (B) TYPE: amino acid
174         (D) TOPOLOGY: linear
176     (ii) MOLECULE TYPE: protein
178     (ix) FEATURE:
179         (A) NAME/KEY: misc_feature
180         (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"
182     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
184 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
185 1      5      10      15
187 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
188      20      25      30
190 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
191      35      40      45
193 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
194      50      55      60
196 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
197 65      70      75      80

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199 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
200      85      90      95
202 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
203      100      105      110
205 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
206      115      120      125
208 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
209      130      135      140
211 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
212 145      150      155      160
214 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
215      165      170      175
217 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
218      180      185      190
220 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
221      195      200      205
223 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
224      210      215      220
226 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
227 225      230      235      240
229 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
230      245      250      255
232 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
233      260      265      270
235 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
236      275      280      285
238 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
239      290      295      300
241 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
242 305      310      315      320
244 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
245      325      330      335
247 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
248      340      345      350
250 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
251      355      360      365
253 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
254      370      375

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256 (2) INFORMATION FOR SEQ ID NO: 3:

258 (i) SEQUENCE CHARACTERISTICS:

259 (A) LENGTH: 1418 base pairs

260 (B) TYPE: nucleic acid

261 (C) STRANDEDNESS: single

262 (D) TOPOLOGY: linear

264 (ii) MOLECULE TYPE: protein

266 (ix) FEATURE:

267 (A) NAME/KEY: CDS

268 (B) LOCATION: 124..1266

270 (ix) FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\50013825_1.RTF

Output Set: N:\CRF3\02142002\J053753.raw

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271      (A) NAME/KEY: misc_feature
272      (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
276 GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCACCCG GCTGCGCACG GCCTGTCCGC      60
278 TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC      120
280 ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT      168
281      Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
282      1          5          10          15
284 CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC      216
285 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
286      20          25          30
288 TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG      264
289 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
290      35          40          45
292 GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC      312
293 Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
294      50          55          60
296 TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC      360
297 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
298      65          70          75
300 TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA      408
301 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
302      80          85          90
304 GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA      456
305 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
306      100         105         110
308 AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC      504
309 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
310      115         120         125
312 GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG      552
313 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
314      130         135         140
316 GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG      600
317 Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu
318      145         150         155
320 GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG      648
321 Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln
322      160         165         170
324 GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG      696
325 Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu
326      180         185         190
328 TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG      744
329 Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu
330      195         200         205
332 AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT      792
333 Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro
334      210         215         220
336 TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC      840
337 Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/053,753

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TIME: 16:04:12

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:886 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:907 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:928 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:949 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:970 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17